

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- 5 (i) APPLICANT: Michael A. Apicella
Melvin G. Sunshine
Na-Gyong Lee
Bradley Gibson
Rasappa Arumugham
- 10 (ii) TITLE OF INVENTION: Non-Toxic Mutants of Pathogenic Gram-Negative Bacteria
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
- (B) STREET: 1800 One M&T Plaza
- (C) CITY: Buffalo
- (D) STATE: New York
- 20 (E) COUNTRY: United States
- (F) ZIP: 14203-2391
- (v) COMPUTER READABLE FORM:
- 25 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
- (D) SOFTWARE: Wordperfect for Windows 5.1
- 30 (vi) APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (vii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Nelson, M. Bud
- (B) REGISTRATION NUMBER: 35,300
- 35 (C) REFERENCE DOCKET NUMBER: 22244.0002
- (viii) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (716) 856-4000
- (B) TELEFAX: (716) 849-0349
- 40 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 969 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: yes
- (iv) ORIGINAL SOURCE:
- (A) ORGANISM: *H. influenzae*
- 50 (B) STRAIN: 2019
- (C) CELL TYPE: bacterium
- (v) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAACTACGC CCCTAACTTA CGTGGAAAGA ACA ATG AAA AAC 42

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		Met Lys Asn
		1
5	GAA AAA CTC CCT CAA TTT CAA CCG CAC TTT TTA GCC CCA 81 Glu Lys Leu Pro Gln Phe Gln Pro His Phe Leu Ala Pro 5 10 15	
10	AAA TAC TGG CTT TTT TGG CTA GGC GTG GCA ATT TGG CGA 120 Lys Tyr Trp Leu Phe Trp Leu Gly Val Ala Ile Trp Arg 20 25	
15	AGT ATT TTA TGT CTT CCC TAT CCT ATT TTG CGC CAT ATT 159 Ser Ile Leu Cys Leu Pro Tyr Pro Ile Leu Arg His Ile 30 35 40	
20	GGT CAT GGT TTC GGT TGG CTG TTT TCA CAT TTA AAA GTG 198 Gly His Gly Phe Gly Trp Leu Phe Ser His Leu Lys Val 45 50 55	
25	GGT AAA CGT CGA GCT GCC ATT GCA CGC CGT AAT CTT GAA 237 Gly Lys Arg Arg Ala Ala Ile Ala Arg Arg Asn Leu Glu 60 65	
30	CTT TGT TTC CCT GAT ATG CCT GAA AAC GAA CGT GAG ACG 276 Leu Cys Phe Pro Asp Met Pro Glu Asn Glu Arg Glu Thr 70 75 80	
35	ATT TTG CAA GAA AAT CTT CGT TCA GTA GGC ATG GCA ATT 315 Ile Leu Gln Glu Asn Leu Arg Ser Val Gly Met Ala Ile 85 90 95	
40	ATC GAA ACT GGC ATG GCT TGG TTT TGG TCG GAT TCA CGT 354 Ile Glu Thr Gly Met Ala Trp Phe Trp Ser Asp Ser Arg 100 105	
45	ATC AAA AAA TGG TCG AAA GTT GAA GGC TTA CAT TAT CTA 393 Ile Lys Lys Trp Ser Lys Val Glu Gly Leu His Tyr Leu 110 115 120	
50	AAA GAA AAT CAA AAA GAT GGA ATT GTT CTC GTC GGC GTT 432 Lys Glu Asn Gln Lys Asp Gly Ile Val Leu Val Gly Val 125 130	
55	CAT TTC TTA ACG CTA GAA CTT GGC GCA CGC ATC ATT GGT 471 His Phe Leu Thr Leu Glu Leu Gly Ala Arg Ile Ile Gly 135 140 145	
60	TTA CAT CAT CCT GGC ATT GGT GTT TAT CGT CCA AAT GAT 510 Leu His His Pro Gly Ile Gly Val Tyr Arg Pro Asn Asp 150 155	
65	AAT CCT TTG CTT GAT TGG CTA CAA ACA CAA GGC CGT TTA 549 Asn Pro Leu Pro Asp Trp Leu Gln Thr Gln Gly Arg Leu 160 165 170	

CGC TCC AAT AAA GAT ATG CTT GAT CGT AAA GAT TTA CGC 588
 Arg Ser Asn Lys Asp Met Leu Asp Arg Lys Asp Leu Arg
 175 180 185

5 GGA ATG ATC AAA GCT TTA CGC CAC GAA GAA ACC ATT TGG 627
 Gly Met Ile Lys Ala Leu Arg His Glu Glu Thr Ile Trp
 190 195

10 TAT GCG CCT GAT CAC GAT TAC GGC AGA AAA AAT GCC GTT 666
 Tyr Ala Pro Asp His Asp Tyr Gly Arg Lys Asn Ala Val
 200 205 210

15 TTT GTT CCT TTT TTT GCA GTA CCT GAC ACT TGC ACT ACT 705
 Phe Val Pro Phe Phe Ala Val Pro Asp Thr Cys Thr Thr
 215 220

20 ACT GGT AGT TAT TAT TTA TTG AAA TCC TCG CAA AAC AGC 744
 Thr Gly Ser Tyr Tyr Leu Leu Lys Ser Ser Gln Asn Ser
 225 230 235

25 AAA GTG ATT CCA TTT GCG CCA TTA CGC AAT AAA GAT GGT 783
 Lys Val Ile Pro Phe Ala Pro Leu Arg Asn Lys Asp Gly
 240 245 250

30 TCA GGC TAT ACC GTG AGC ATT TCA GCG CCT GTT GAT TTT 822
 Ser Gly Tyr Thr Val Ser Ile Ser Ala Pro Val Asp Phe
 255 260

35 ACA GAT TTA CAA GAT GAA GTA GCG ATA GCT GTG CGA ATG 861
 Thr Asp Leu Gln Asp Glu Val Ala Ile Ala Val Arg Met
 265 270 275

40 AAT CAA ATC GTT GAA AAG GAA ATC ATG AAG GGC ATA TCA 900
 Asn Gln Ile Val Glu Lys Glu Ile Met Lys Gly Ile Ser
 280 285

45 CAA TAT ATG TGG CTA CAT CGT CGT TTT AAA ACA CGC CCC
 Gln Tyr Met Trp Leu His Arg Arg Phe Lys Thr Arg Pro
 290 295 300

50 GAT GAA AAT ACG CCT AGT TTA TAC GAT TAA 969
 Asp Glu Asn Thr Pro Ser Leu Tyr Asp
 305 310

(3) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single-stranded
 (D) TOPOLOGY: linear
 (ii) ORIGINAL SOURCE:
 (A) ORGANISM: *H. influenzae*
 (B) STRAIN: 2019

(iii) IMMEDIATE SOURCE: synthesized
(iv) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCAATATGGC GCAAAATAGG ATAGGGAAGA C 31

5

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 nucleotides
(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single-stranded
(D) TOPOLOGY: linear

(ii) ORIGINAL SOURCE:

- (A) ORGANISM: *H. influenzae*

(iii) FEATURE:

15 (A) OTHER INFORMATION: uptake sequence for transformation

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGTGCGGT 9

20

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 nucleotides
(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single-stranded
(D) TOPOLOGY: linear

(ii) FEATURE:

- (A) OTHER INFORMATION: hybridizes to TNF α mRNA

30 (iii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCTCTCAGC TCCACGCCAT TGGCCAGGAG 30

35

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single-stranded
(D) TOPOLOGY: linear

(ii) FEATURE:

40 (A) OTHER INFORMATION: does not hybridize to TNF α mRNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCCTGGCCA ATGGCGTGG A GCTGAGAGAT 30